**db\_open()**

Parameters: None

Function: Opens a connection to the database

Returns: Nothing

**db\_close()**

Parameters: None

Function: Closes the connection to the database

Returns: Nothing

**get\_snp\_by\_id (querystring)**

Parameters: <querystring>: Type string. The SNP to search for.

Function: Queries the database using the search term <querystring> against the column *snp\_id* using the where clause WHERE snp\_id LIKE ‘<querystrting>”

Returns: Dataframe of results, or an empty dataframe if there are no results

**get\_snp\_by\_gene (querystring)**

Parameters: <querystring>: Type string. The mapped gene string to search for.

Function: Queries the database using the search term <querystring> against the column *mapped\_gene* using the where clause WHERE mapped\_gene LIKE ‘<querystring >”

Returns: Dataframe of results, or an empty dataframe if there are no results

**get\_snp\_by\_coordinates (chromosome, start, end)**

Parameters: <chromosome>: Type string. The chromosome string to search for.

<start>: Type integer. The starting position to search for.

<end>: The integer. The end position to search for.

Function: Queries the database using the search term < chromosome > against the column *chromosome* and where the column *position* is between <start> and <end>. The where clause used is WHERE chromosome = <chromosome> AND position >= <start> AND position <= <end>

Returns: Dataframe of results, or an empty dataframe if there are no results